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**TABLE I**  
Prevention/Reduction of Proteinuria by Treatment  
With Anti-C5 Antibodies

	Before Treatment	After Treatment
	Urine Protein (mg/dL)	Urine Protein (mg/dL)

**PBS Control**

mouse A	none	100
mouse B	none	500
mouse C	none	500
mouse D'	trace	trace
mouse E	100	100

**Anti-C5 Treated**

mouse 1	none	none
mouse 2	none	30
mouse 3	30	trace
mouse 4	30	30
mouse 5	30	30
mouse 6	100	30

\* Mouse D had more than 500mg/dL urine glucose after treatment

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Evans, Mark J.  
Matis, Louis A.  
Mueller, Eileen Elliott  
Nye, Steven H.  
Rollins, Scott  
Rother, Russell P.  
Springhorn, Jeremy P.  
Squinto, Stephen P.  
Thomas, Thomas C.  
Wang, Yi  
Wilkins, James A.

(ii) TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR THE TREATMENT  
OF GLOMERULONEPHRITIS AND OTHER INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 1951 Burr Street  
(C) CITY: Fairfield  
(D) STATE: Connecticut  
(E) COUNTRY: USA  
(F) ZIP: 06430

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage  
(B) COMPUTER: Macintosh Cetris 610  
(C) OPERATING SYSTEM: System 7  
(D) SOFTWARE: WordPerfect 3.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/236,208  
(B) FILING DATE: 02-MAY-1994

(viii) ATTORNEY/AGENT INFORMATION:  
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(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (203) 255-1400  
(B) TELEFAX: (203) 254-1101

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(A) DESCRIPTION: KSSKC peptide  
(ii) HYPOTHETICAL: No  
(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser ...  
5 10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser  
15 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1658 Amino Acids  
(B) TYPE: Amino Acid

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(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(A) DESCRIPTION: Pro-C5 Polypeptide  
(iii) HYPOTHETICAL: No  
(iv) ANTISENSE: No  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens  
(x) PUBLICATION INFORMATION:  
(A) AUTHORS: Haviland, D.L.  
Haviland, J.C.  
Fleischer, D.T.  
Hunt, A.  
Wetsel, R.A.  
(B) TITLE: Complete cDNA Sequence of Human Complement Pro-C5  
(C) JOURNAL: Journal of Immunology  
(D) VOLUME: 146  
(F) PAGES: 362-368  
(G) DATE: 1991

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Leu Gly Ile Leu Cys Phe Leu  
-15 -10

Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val  
-5 -1 5

Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn  
10 15 20

Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala  
25 30

Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr

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35

40

45

Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln  
50                       55                       60

Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly  
65                       70                       75

Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser  
80                       85                       90

Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp  
95                       100

Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr  
105                      110                       115

Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp  
120                      125                       130

Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile  
135                      140                       145

Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp  
150                      155                       160

His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser  
165                      170

Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys  
175                      180                       185

Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys  
190                      195                       200

Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu  
205                      210                       215

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Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile  
220 225 230

Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu  
235 240

Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys  
245 250 255

Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr  
260 265 270

Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu  
275 280 285

Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu  
290 295 300

Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser  
305 310

Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys  
315 320 325

Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro  
330 335 340

Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln  
345 350 355

Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val  
360 365 370

Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser  
375 380

Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly  
385 390 395

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Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val  
400 405 410

Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu  
415 420 425

Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser  
430 435 440

Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn  
445 450

His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val  
455 460 465

Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn  
470 475 480

Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr  
485 490 495

Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile  
500 505 510

Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val  
515 520

Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser  
525 530 535

Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln  
540 545 550

Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro  
555 560 565

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Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser  
570 575 580

Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val  
585 590

Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe  
595 600 605

Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Leu  
610 615 620

Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu  
625 630 635

Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro  
640 645 650

Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys  
655 660

Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys  
665 670 675

Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr  
680 685 690

Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys  
695 700 705

Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu  
710 715 720

Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu  
725 730

His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg  
735 740 745

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Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val  
750 755 760

Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu  
765 770 775

Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly  
780 785 790

Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp  
795 800

Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly  
805 810 815

Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr  
820 825 830

Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly  
835 840 845

Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr  
850 855 860

Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser  
865 870

Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly  
875 880 885

Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys  
890 895 900

Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val  
905 910 915

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Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly  
920 . . . . . 925 . . . . . 930

Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg  
935 . . . . . 940

Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile  
945 . . . . . 950 . . . . . 955

Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile-Leu Ser Ala  
960 . . . . . 965 . . . . . 970

Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro  
975 . . . . . 980 . . . . . 985

Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val  
990 . . . . . 995 . . . . . 1000

Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn  
1005 . . . . . 1010 . . . . .

Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys  
1015 . . . . . 1020 . . . . . 1025

Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg  
1030 . . . . . 1035 . . . . . 1040

Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala  
1045 . . . . . 1050 . . . . . 1055

Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln  
1060 . . . . . 1065 . . . . . 1070

Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn  
1075 . . . . . 1080 . . . . .

Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly  
1085 . . . . . 1090 . . . . . 1095 . . . . .

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Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gin  
1100 1105 . . . 1110 . .  
  
Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu  
1115 . . 1120 . . . 1125  
  
Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile  
1130 . . 1135 . . 1140  
  
Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp  
1145 . . 1150  
  
Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe  
1155 1160 . . 1165 .  
  
Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys  
1170 . . 1175 . . 1180  
  
Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg  
1185 . . 1190 . . 1195  
  
Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp  
1200 . . 1205 . . 1210  
  
Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr  
1215 . . 1220  
  
Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu  
1225 . . 1230 . . 1235  
  
Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val  
1240 . . 1245 . . 1250  
  
Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe  
1255 . . 1260 . . 1265

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Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr  
1270 1275 1280

Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp  
1285 1290

Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr  
1295 1300 1305

Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val  
1310 1315 1320

Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser  
1325 1330 1335

Gly Leu Ala Thr Val His Val Thr Val Val His Lys Thr  
1340 1345 1350

Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp  
1355 1360

Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn  
1365 1370 1375

Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro  
1380 1385 1390

Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met  
1395 1400 1405

Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp  
1410 1415 1420

Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp  
1425 1430

Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser  
1435 1440 1445

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Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe  
1450                    1455                    1460

Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr  
1465                    1470                    1475

Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe  
1480                    1485                    1490

Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly  
1495                    1500

Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln  
1505                    1510                    1515

Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln  
1520                    1525                    1530

Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser  
1535                    1540                    1545

Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys  
1550                    1555                    1560

Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala  
1565                    1570

Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys  
1575                    1580                    1585

Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met  
1590                    1595                    1600

Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg  
1605                    1610                    1615

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Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp  
1620. 1625 . . . . . 1630 . . . . .  
Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala  
1635 . . . . . 1640 . . . . .  
Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys  
1645 . . . . . 1650 . . . . . 1655 . . . . .

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4059 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

- (ii) MOLECULE TYPE: Other nucleic acid
  - (A) DESCRIPTION: Apex-1 Eukaryotic Expression Vector

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGCGTTGAC ATTGATTATT GACTAGTTAT TAATCTAAAT CAATTACGGG . . . 50  
GTCATTTAGT CATAGGCCAT ATATGGAGTT CGCGGTACAA TAACCTACCG . . . 100  
TAATATGGCCC CGGCCTGGCTG ACCGCCCCAAC GACCCCGGGCC. CATTGACGTC . . . 150  
ATAATATGACG TATGTTCCCA TAGTAAACGCC ATATGGGACT TTCCATTGAC . . . 200  
GTCATATGGGT GGACTATTTA CGGTAAACTG CCCACTTGGC AGTACATCAA . . . 250  
GTGTATCATCA TGCCAAGTAC GCCCCCTATT GACGTCAATG ACGGTTAAATG . . . 300  
GCCCGCCCTGG CATTATGCCA AGTACATGAC CTTATGGAC TTTCTACTT . . . 350  
GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT . . . 400

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TGGCAGTACA TCAATGGCGG TGGATAGCGG TTTGACTCAC GGGGAATTCC 450  
AAGTCCTCAC CCCATTGACG TCAATGGAG TTTGTTTTGG CACCAAAATC 500  
AACCGGAACTT TCCAAAATGT CGTAACAACG CGGCCCTTATG GACGCAAATG 550  
GGCGGTAGGC GTGTACGGTG GGAGGTCTAT ATAAAGCAGAG CTCTTTAGT 600  
GAACCGTCAG AATTCTGTTG GGCTCGCGGT TGATTACAAA CTCTTCGGG 650  
TCTTTCAGT ACTCTTGGAT CGGAAACCGG TCGGCCCTCG AACGGTACTC 700  
CGCCACCGAG GGACCTGACG GACTCCGAT CGACCGGATC GGAAACCTC 750  
TCGACTGTTG GGTTGAGTAC TCCCTCTCAA AAAGGGGGCAT GACTCTGGG 800  
CTAAGATTGT CAGTTTCCAA AAACGAGGGAG GATTGATAT TCACCTGGCC 850  
CGCCGGTAGT CCTTTGAGGG TGGCCCGCTC CACTTGGTCA GAAAAGACAA 900  
TCCTTTTGTG GTCAAGCTTG AGGTGTTGGCA GGCTTGAGAT CTGGCCATAC 950  
ACTTGAGTGA CAATGACATC CACTTTGGCT TTCTCTCCAC AGGTGTCAC 1000  
TCCCCAGTCC AACTGCAAGGT CGACCGGCTT GGTAACCGAGC TOGGATCCAC 1050  
TAGTAACGGC CGCCAGTGTG CTGGAATTCT GCAGATATCC ATCACACTGG 1100  
CGGCCGCTCG AGCATGACATC TAGAACTTGT TTATTGAGC TTATAATGGT 1150  
TACAAATAAA GCAATAGCAT CACAAATTTC ACAAAATAAG CATTTCCTTC 1200  
ACTGCATCTC AGTTGTTGGTT TGTCCAACCT CATCAATGTA TCTTATCATG 1250  
TCTGGATGCA TCCCCCCATG GTATCAACGC CATAATTCTA TTTACAGTAG 1300  
GGACCTCTTC GTTGTTGAGG TACCGCTGTA TTCCTAGGGA AATAGTAGAG 1350

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GCACCTTGAA	CTGTCCTGCA	CAGCCATATA	'GCCCGCGCTG	TTCGACTTAC	1400
AAACACAGGC	ACAGTACTGA	CAAACCCATA	CACCTCCTCT	.GAAATACCCA	1450
TAGTTGCTAG	GGCTGTCCTCC	GAACCTATTA	CACCCCTCAA	AGTCAGAGCT	1500
GTAATTTCGC	CATCAAGGGC	ACCGAGGGCT	TCTCCAGATA	.AAATAGCTTC	1550
TGCCGAGAGT	CCCCTAAGGG	TAGACACTTC	AGCTAATCCC	TCGATGAGGT	1600
CTACTAGAAT	AGTCAGTGGC	GCTCCCATTT	TGAAATTCA	CITACTTGAT	1650
CAGCCTTCAGA	AGATGGCGGA	GGGCCTCCAA	CACAGTAATT	TTCCCTCCOGA	1700
CTCTTAAAT	AGAAAATGTC	AGTCAGTTA	AGCAGGAAGT	GGACTAACTG	1750
ACGCAGCTGG	CGCTGCGACA	TCCCTCTTTA	ATTAGTGTGCT	AGGCAACGCC	1800
CTCCTAGAOGG	CCTGTGTTTT	TGCAJAGGGA	AGCAAARGCC	TCTCCACCCA	1850
GGCCTAGAACAT	GTTCACCCCC	AATCATTACT	ATGACAAACAG	CITGTTTTTT	1900
TAGTATTAAG	CAGAGGCCGG	GGACCCCTGG	GGCCCGCTTAC	TCTGGAGAAA	1950
AAGAAGAGAG	GCATTCGAGA	GGCTTCAGA	GGCAACTTGT	AAAAACAGGA	2000
CTGCTCTAT	TTCTGTCACA	CTGCTCTGGCC	CTGTCACAAAG	GTCCAGCACC	2050
TCCATACCCC	CTTTAATANG	CAGTTGGGA	ACGGGTGCGG	GTCTTACCTCC	2100
GCCCCATCCCC	CCCCCTAACTC	CGCCCAAGTTC	CGCCCATTTCT	CGGCCCCATG	2150
GCTGACTAAT	TTTTTTTATT	TATGCAGAGG	CCGAGGCCGC	CTCGGGCTCT	2200
GAGCTATTCC	AGAAGTAGTG	AGGAGGCTTT	TTTGAGGCC	TAGGCTTTG	2250
CAAAAAGGAG	CTCCCCAGCAA	AAGGCCAGGA	AUCGTAAAAA	GGCCGCGTTG	2300

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CTGGCGTTTT TCCATAGGCT CGGCCCGCCT GACGAGCATC ACAAAAATCG	2350
ACGGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAAGG	2400
CGTTTCCCCC TGGAAGCTCC CTGGTGCGCT CTGCTGTTCC GACCCCTGCGG	2450
CITTACCGAT ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC	2500
TCAATGCTCA CGCTGTAGGT ATCTCAGTTC GGTTGAGGTC GTTCGCTCCA	2550
AGCTGGGCTG TGTGCACGAA CCCCCGGTTC AGGCCCCACCG CTGCGCCCTTA	2600
TCCGGTAACT ATOGTCTTGA GTCCAAACCGG GTAAGACACGG ACTTATCGCC	2650
ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCQAGG TATGTAGGCG	2700
GTGCTACAGA GTTCTTGAAG TGGTGGCTTA ACTACGGCTA CACTAGAAGG	2750
ACAGTATTTG GTATCTGCGC TCTGCTGAAG CCAGTTACCT TOGGAAAAAG	2800
AGTTGGTAGC TCTTGATCCG GCACAAACAC CACCGCTGGT AGCGGGTGGTT	2850
TTTTTGTGTC CAAGCAGCAG ATTACCGCCTA GAAAAAAAAGG ATCTCAAGAA	2900
GATCCCTTGA TCTTTCTCAC GGGGTCTGAC GCTCACTTGA ACGAAAACCTC	2950
ACGTTAAGGG ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA	3000
TCCCTTTAAA TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG	3050
TAAACTTGGT CTGACAGGTA CCAATGCTTA ATCAGTGAGG CACCTATCTC	3100
AGCGATCTGT CTATTCGTT CATCCATAGT TGCGCTGACTC CCCGTCGTGT	3150
AGATAACTAC GATAACGGGAG GGCTTACCAT CTGGCCCCAG TGCTGCAATG	3200
ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA	3250

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GGCAGCCCGGA AGGCCCCGAGC GCAGAAAGTGG TTCTGCCACT TTATCCGCGCT .. 3300  
CCATCCAGTC TATTAATTGT TGCCGGGGAAAG CTAGAAGTAAG TAGTTCCCCA .. 3350  
GTTAATAGTT TCGCGAACGT TGTGCAATT GCTACAGGCA TCGTGGGTGTC .. 3400  
ACGCTCGTGC TTTGGTATGG CTTCAATTAG CTCGGGTTC CAACGATCAA .. 3450  
GGCGAGTTAC ATGATCCCCC ATGTTGIGCA AAAAAGCGGT TAGCTCCITC .. 3500  
GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCGCGAGTGT TATPCACTCAT .. 3550  
GGTTATGGCA GCACTGCATA ATTCTCCTAC TGTCACTCCA TCCGTAAGAT .. 3600  
GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCRATTCTG AGAATAGTGT .. 3650  
ATGCGGGCGAC CGAGTTGCTC TTGCCCCGGG TCAATACGGG ATAATACCGC .. 3700  
GCCACATAGC AGAACCTTAA AAGTGCTCAT CATTTGGAAAA CTTTCTTCGG .. 3750  
GGCGAAACTCTCAAGATC TTACCGCTGT TGAGATCCAG TTCGATGTAA .. 3800  
CCCACTCGTG CACCCAACTG ATCTTCAGCA TCCTTTACTT TCACCAGCGT .. 3850  
TTCTGGGTGA GCACAAAACAG GAAGGCAAA TGCCCAAAA AAGGGAAATA .. 3900  
GGCGGACACG GARATGTTGA ATACTCATAC TCTTCCTTT TCAATATTAT .. 3950  
TGAAGCATTG ATCAGGGTTA TTGTCTCAAG AGCGGATACAA TATTGAAATG .. 4000  
TATTTAGRAA AATAAACAAA TAGGGGTTCC GGCGCACATT CCCCGAAAAG .. 4050  
TGCCACCTG .. 4059

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## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8540 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Circular
- (ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Apex-3' Eukaryotic  
Expression Vector

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCCAATA CAAACACAAA GCGCCGCCCTCG TACCAAGGAA GAAGGGGCA 50  
AGATGCCGCTA GTCAGGTTTA GTTCGTCCGG CGGCAGGGGA TCTGTATGGT 100  
GCACTCTCG TACAATCTGC TCTGATGCCG CATACTTAAG CCAGTATCTG 150  
CTCCCCTGCTT GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA GCAAAATTAA 200  
AGACTAACAA AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA 250  
GGGTTAGGG TTTTCCGCTG CTTCGCGATG TACGGGCCAG ATATAACCGT 300  
TGACATTGAT TATTGACTAG TTATAATAG TAATCAATTAA CGGGGTCAATT 350  
AGTTCATAGC CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAATAG 400  
GCCCGCCCTGG CTGACCGCCCC AACGACCCCC GCCCATTGAC GTCAATAATG 450  
ACGTATGTTG CCTTAGTAAAC GCCAATAGGG ACTTTCCATT GACGTCATG 500  
GGTGGACTAT TTACGGTAAA CTGCCCCACTT GGCAGTACAT CAAAGTGTATC 550  
ATATGCCAAG TACGCCCTCT ATTGACGGTCA ATGACGGTAA ATGGCCCGCC 600  
TGGCAATTATG CCCAGTACAT GACCTTATGG GACITTCCTA CTTGGCAGTA 650

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CATCTACGTA TTAGTCATCG CTATTAACCAT GGTGATGCGG TTTTGGCAGT ..700  
ACATCAATGG CGCTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC ..750  
CACCCCCATG ACGTCAATGG GAGTTTGTGTT TGGCACCCAA ATCAACGGGA ..800  
CTTTCCAAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGGCGGT ..850  
GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT ..900  
CAGAATTCTG TTGGGCTCGC GGTTGATTCAC AAACTCTTCG CGGTCTTTCC ..950  
AGTACTCTTG GATCGGAAAC CGCTGGCCCT CGGAACGGTA CTCCGGCAC ..1000  
GAGGGACCTG AGCGAGTCGG CATCGACCGG ATCGGAAAAC CTCTCGACTG ..1050  
TTGGGGTGAG TACTCCCTCT CAAAGCGGG CATGACTTCTG GGGCTAAGAT ..1100  
TGTCACTTTC CAAAAAACGAG GAGGATTGTA TATTCACCTG GCGCGGGGTG ..1150  
ATGCCCTTGA GGGTGGCGCG GTCGCATCTGG TCAGAAAAGA CAACTTTTT ..1200  
GTTGTCAAAGC TTGAGGTGTG GCAGGCTTGA GATCTGGCCA TACACTTGAG ..1250  
TGACAAATGAC ATTCACCTTG CCTTCTCTC CACAGGTGTC CACTCCAGG ..1300  
TCCAACTGCA GGTGCGACCGG CTTGGTACCGG AGCTCGGATC CTCTAGAGTC ..1350  
GACCTGCAAGG CATGCAAGCT TGGCACTGGC CGTCGTTTAA CAACGTGTG ..1400  
ACTGGGGAAA CCCTGGCGTT ACCCAACTTA ATCCGCTTGC AGCACATCCC ..1450  
CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCCAGACAT ..1500  
GATAAGATAAC ATTGATGAGT TTGGACAAAC CACRACTAGA ATGCAAGTGA ..1550  
AAAAATGCTT TATTTGTGAA ATTTGTGATG CTATTCGCTT ATTTGTAAACC ..1600

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ATTATAAGCT GCAATAAACA AGTTAACAAAC AACAAATGCA TTCATTITAT 1650  
GTTTCAGGGT CAGGGGGGAG TGTGGGAGGT TTTTAAAGC AAGTAAAACC 1700  
TCTACAAATG TGGTATGGT GATTATGATC CCCAGGAAGC TCCCTCTGTGT 1750  
CCTCATAAAC CCTAACCTTC TCTACTTGAG AGGACATTCC AATCATAGGC 1800  
TGGCCATCCA CCCTCTGTGT CCTCCCTGTT ATTAGGTAC TTAACAAAAA 1850  
GGAAATTTGGG TAGGGGTTTT TCACAGACCG CTTTCTAAGG GAAATTTAA 1900  
AATATCTGGG AAGTCCCTTC CACTGCTGTG TTCCAGAAAGT GTGGTAAAC 1950  
AGCCCACAAA TGTCACACG AGAAACATAC AAGCTGTCAAG CTTCGCACAA 2000  
GGGCCCAACA CCCTGCCTCAT CAAGAAGCAC TGTGGGTGCT GTGTTAGTAA 2050  
TGTGCAAAAC AGGAGGCACA TTTCCCCCAC CTGTGTAGGT TCCAAATAT 2100  
CTAGTGTGTT CTTTTTACT TGGATCAGGA ACCCCAGCACT CCACGGATA 2150  
AGCATTATCC TTATCCAAAA CAGCCTTGTC GTCACTGTTC ATCTGCTGAC 2200  
TGTCACTGT AGCATTTTTG GGGGTTACAG TTTGAGCAGG ATATTTGGTC 2250  
CTGTGTTTG CTAACACACC CTGCAGCTCC AAAGGTTCCC CACCAACAGC 2300  
AAAAAAATGA AATTTGACCA CTGAAATGGG TTTTCCAGCA CCATTTTCAT 2350  
GAGTTTTTG TGTCCTTGAA TGCAAGTTA ACATAGCAGT TACCCCAATA 2400  
ACCTCAGTTT TAACAGTAAC AGCTTCCCCAC ATCAAATAT TTCCACAGGT 2450  
TAAGTCTCTCA TTGTAGAAT TGCCAGCAC AGTGGTCGAC CCTGTGGATG 2500  
TGTGTCACCT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT 2550

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ATGCAAAAGCA TGCACACTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC .2600  
AGGCTCCCCA GCAGGGCAGAA .GATGCAAGG CATGCATCTC AATTAGTCAG 2650  
CAACCATAGT CCGGCCCCCTA ACTCCGCCA TCCCGCCCT AACTCCGCC .2700  
AGTTCCGCCA ATTCTCCGCC CCATGGCTGA CTAAATTTTT TTATTTATGC 2750  
AGAGGGCCAG GCGCGCCCTGG CCTCTGAGCT ATTCAGAAG TAGTGAGGAG 2800  
GCTTTTTTGG AGGCTTAGGC TTTTGCAAAA GCTTACCATG ACCGAGTACA 2850  
ACCCCTACGGT GCGCCCTGCCA .ACCCGGAGCC AGCTCCCCCG .GGCCCTACCG 2900  
ACOCTCGCG CGCGCGTTGC CGACTACCCC GCCACGCC ACACCGTGA 2950  
CCCGGACCG CACATGAGC GGGTCACOGA GCTGCAAGAA CTCTTCTCA 3000  
CGCGCGTCCGG .GCTCGACATC CGCAAGGTTG GGTGCGGGA CGACCGCGCC .3050  
GCGGTGGCGG TCTGGACCAC GCGGGAGAGC GTCGAAGCGG .GGGCGGTGTT 3100  
CGCCGAGATC GGCCCGCGCA TGGCCGAGTT GAGCGGTCC .CGGCTGGCCG 3150  
CGCACCAACA GATGGAAGGC CTCCTGGGCGC CGCACCGGCC CAAGGAGCCC .3200  
GCCTGGTTCC TGGCCACCGT CGCGCTCTCG CGCGACCCACC AGGGCAAGGG 3250  
TCTGGGCAGC GCCTGCTGTC TCCCCGGAGC GGAGGGGGCC .GAGCGCCCG 3300  
GGGTGCGCCG CTTCTGGAG ACCTCCGGGC CGCGCAACCT .CCCTTCTAC 3350  
GAGCGGGCTG GCTTCACCGT .CACCGCGCGAC GTCGAGTGCC .CGAAGGACCG .3400  
CGCGACCTGG TGCATGACCC GCAAGGGCGG TGCGTGACCG CGCGCCCG 3450  
ACCCGGAGCG CGCGACCGA AGGAGCGCAC GACCCCCATGC ATCGATAAAA 3500

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TAAAAGATT TATTTAGTCT CCAGAAAAAG GGGGAATGA AAGACCCAC 3550  
CTGTTAGTTT GGCAAGCTAC AACTTGTTA TTGCAGCTTA TAATGGTTAC 3600  
AAATAAACCA ATAGCATCAC AAATTTACAA AATAAAGCAT TTTTTTCACT 3650  
GCATTCTAGT TGTGGTTTG CCAAACTCAT CAATGTATCT TATCATGTCT 3700  
GGATCGATCC CGCCATGGTA TCAACGCCAT ATTTCATTT ACAGTAGGGA 3750  
CCTCTTCGTT GTGTTAGGTAC CCCGGGTTCG AAATCGAATT CGCCAATGAC 3800  
AAGACCCCTGG CGGGGGTTTG TGTCATCATCA GAACTAAAGA CATGCCAATA 3850  
TATTTCTTCC GGGGACACCG CCAGCAAAAC CGAGCAACGG GCCACGGGGA 3900  
TGAAGCNGCC CGGGGGCACC TCGCTAACGG ATTCAACCACT CCAAGAATTG 3950  
GAGCCATCA ATTCTTGCGG AGAACTGTGA ATGCGAAAC CAACCCCTTGG 4000  
CAGAACATAT CCATCGCGTC CGCCATCTCC AGCAGCCGCA CGCGCGCAT 4050  
CTCGGGGCCGG ACGCCGCTGGG CTACGCTCTG CTGGCGTTCG CGACGCGAGG 4100  
CTGGATGGCC TTCCCCATTA TGATTCCTCT CGCTTCGGC GGCACTGGGA 4150  
TGCCCCCGTT GCAGGCCATG CTGTCCAGGC AGGTAGATGA CGACCATCAG 4200  
GGACAGCTTC AAGGATGCT CGCGGCTCTT ACCAGCGCCA GCAAAAGGCC 4250  
AGGAACCGTA AAAAGGCGC GTTGCTGGCG TTTTCCATA GGCTCCGCC 4300  
CCCTGACGAG CATCACAAAA ATGAGACGCTC AAGTCAGAGG TGGCGAAACC 4350  
CGACAGGACT ATARAGATAC CAGGGCTTTC CCCCTGGAAG CTCCCTCGTG 4400  
CGCTCTCTG TTCCGACCCCT GCGGCTTACCG GGATAACCTGT CGGCCTTTCT 4450

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CCCTTCGGGA AGCGTGGGCG TTTCTCATAG CTCACGGCTGT AGGTATCTCA 4500  
GTTCGGTGTA GGTGCGTTGCC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC 4550  
GTTCAGCCCG ACCCGCTGGCG CTTATCCGGT AACTATGTC TTGAGTCCAA 4600  
CCCGGTAAAGA CACGACTTAT CGCCACTGGC ASCAGCCACT GGTAACAGGA 4650  
TTAGCAGAGC GAGGTATGTA GGCCTGTGCTA CAGAGTTCTT GAAGTGGTGG 4700  
CTCTAATACCG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT 4750  
GAAGCCAGTT ACCTTCGGAA AAGAGTTGG TAGCTCTTGA TCCGGCAAAAC 4800  
AAACCACCGC TGGTAGCGGT GGTTTTTTG TTTGCAAGCA GCAGATTACG 4850  
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTAGATCTTT CTACGGGOTC 4900  
TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTG GTCATGGAGT 4950  
TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTTAAA ATGAAGTTTT 5000  
AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG 5050  
CTTAATCAGT GAGGCACCTA TCTCACGCGAT CTGTCTTATTT CGTTCATCCA 5100  
TAGTTGCCCTG ACTCCCCGTC GTGTAGATAA CTACGATAAG CGAGGGCTTA 5150  
CCATCTGGCC CGAGTCTGTC AATGATACCG CGAGACCCAC GCTCACCGC 5200  
TCCAGATTTA TCAGCAATAA ACCGCCAGC CGGAAGGGCC GAGCGCAGAA 5250  
GTGGTCTGCA AACTTTATCC GCGCTCATCC AGTCTATTAA TTGTTGCCGG 5300  
GAAGCTAGAG TAATGAGTTC GCCAGTTAT AGTTGCGCA ACOTTGTTGC 5350  
CATTGCTGCA GGCATCGTGG TGTCACTGCTC GTGCGTTGGT ATGGCTTCAT 5400

TCAGCTCCGG TTCCCCACGA TCAAGGCGAG TTACATGATC CCCCATGTG 5450  
TGCAAAAG CGGTTAGCTC CTTGGTCTC CGGATCGPTG TCAGAAGTAA 5500  
GTTGGCCGCA GTGTTATCAC TCATGTTAT GGCAGCACTG CATAATTCTC 5550  
TTACTGTCAT GCCATCGTA AGATGCTTT CTGTGACTGG TGAGTACTCA 5600  
ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC 5650  
GGCGTCAACA CGGGATAATA CGCGGCCACA TAGCAGAACT TTAAAAGTGC 5700  
TCATCATGG AAAACGTTCT TGGGGGGAA AACTCTCAG GATCTTACCG 5750  
CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC 5800  
AGCATCTTT ACTTTCACCA GCCTTTCTGG GTGAGCAAAA ACAGGAAGGC 5850  
AAAATGCCG AAAAAGGGAA ATAAGGGCGA CACGGAAATG TTGAACTCTC 5900  
ATACTCTTC TTTTCAATA TTATTGAAAGC ATTTATCAGG GTTATTGTCT 5950  
CATGAGCGGA TACATAITTG ATGTTATTTA GAAAAATAAA CAATAGGGG 6000  
TTCCGGCGAC ATTTCCCCA AAAGTGCAC CTGACGCTCA AGAAACCAT 6050  
ATATATCATGA CATTAACTCA TAAAAATAGG CGTATCACGA GGCCCTTTCG 6100  
TCTTCAGAA TTCTCATGGT TGACAGCTCA TCCTGAGACAT CATCGTGCT 6150  
GTTGGTGTAT TTCTGGCCAT CTGTCTGTC ACCATTTGCG CCTCTCCAAC 6200  
ATGGGGCAAT TGGGCATACC CAGTGTGTCA CGTCACTCAG CTCCGGCGTC 6250  
AACACCTTCT CGCGTTGGAA AACATTAGCG ACATTTACCT GGTGAGCAAT 6300  
CAGACATGCG ACGGCTTAG CCTGGCTCC TTAAATTCAC CTAAAGATGG 6350

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GAGCAACCAG CAGGAAARAGG ACAACCGAGCG AAAATTCCAGG CCCCTTGGG 6400  
AGGTGGCCGC ATATGCAAAG GATAGCCTAC CCACTCTACT ACTGGGTTATC 6450  
ATATGCTGAC TGTATATGCA TGAGGATAGC ATATGCTACC CGGATACAGA 6500  
TTAGGATAGC ATATACTTAC CAGATATAGA TTAGGATAGC ATATGCTACC 6550  
CAGATATAGA TTAGGATAGC CTATGCTACC CAGATATATAA TTAGGATAGC 6600  
ATATACTTAC CAGATATAGA TTAGGATAGC ATATGCTACC CAGATATAGA 6650  
TTAGGATAGC CTATGCTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6700  
CAGATATAGA TTAGGATAGC ATATGCTATC CAGATATTTG GGATGATAT 6750  
GCTACCCAGA TATAAAATTAG GATAGCATAT ACTACCCATAA TCTCTATTAG 6800  
GATAGCATAT GCTACCCAGA TACAGATTAG GATAGCATAT ACTACCCAGA 6850  
TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT .6900  
GCTACCCAGA TATAAAATTAG GATAGCATAT ACTACCCAGA TATAGATTAG 6950  
GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT GCTACCCAGA 7000  
TATAGATTAG GATAGCATAT GCTATCCAGA TATTTGGGTA GTATATGCTA 7050  
CCCATGGCAA CATTAGCCCCA CGGTGCTCTC AGCGACCTCG TGAATATGAG 7100  
GACCAACAAAC CCTGTGCTTG GCGCTCAGGC GCAAGTGCTGT GTAATTGTC 7150  
CTCCAGATCG CAGCAATCGC GCCCCATATCT TGGCCCCGCC ACCTACTTAT 7200  
GCAGGGTATTC CCCGGGGTGC CATTAGTGGT TTGTGGGCA AGTGGTTGTA 7250  
CCGCAGTGGT TAGCGGGGTT ACAATCAGCC AAGTTATTAC ACCCTTATTT 7300

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TACAGTCCAA AACCGCAGGG CGGCGTGTGG GGGCTGACGC GTGGCCCCAC 7350  
TCCACAAATT CAAAAAAAAG AGTGGCCACT TGTCTTTGTT TATGGGCCCC 7400  
ATTGGCGTGG AGCCCCGTTT AATTTTCGGG GGTGTTAGAG ACAACCAGTG 7450  
GAGTCGGCTG CTGTCGGCTG CCACCTCTCTT TCCCCTTGTG ACAAATAGAG 7500  
TGTAAACACA TGTTTACCT GTCTTGGTCC CTGCTGGGA CACATCTAA 7550  
TAACCCAGT ATCAATTTGC ACTAGGTTA TGTGTTGCCC ATAGCCATAA 7600  
ATTCGCTGTA GATGGACATC CAGTCCTTAC GGCTTGTCCC CACCCCATGG 7650  
ATTTCTATTG TAAAGATTT TCAGAATTT TCATTCCTAC ACTAGTATTT 7700  
ATTGCCAAG GGGTTTGTGA GGGTTATATT GGTTGTCATAG CACAATGCCA 7750  
CCACTGAAACC CCCCTCTCAA ATTTTATTCT GGGGGCGTCA CCTGAAACCT 7800  
TGTTCGAG CACCTCACAT ACACCTTACT GTTCACAACCT CAGCAGTTAT 7850  
TCTATTAGCT AAACGAAGGA GAATGAAGAA GCAGGGGAG ATTCAAGGAGA 7900  
GTTCACTGCC CGCTCCTTGA TCTTCAGCCA CTGCCCCCTGT GACTAAATG 7950  
GTTCACTACC CTGGTGGAAAT CCTGACCCCA TGTAATAAAA ACCGGTACAG 8000  
CTCATGGGGT GGGAGATATC GCTGTTCCCTT AGGACCCCTT TACTAACCT 8050  
AATTGATAG CATACTGCTTC CCGTTGGTAA ACATATGCTA TTGAAATTAGG 8100  
GTTAGCTGG ATAGTATATAA CTACTACCCG GGAAGGATAT GCTAACCCGTT 8150  
TAGGGTTAAC AAGGGGGCCCT TATAAACACT ATTGCTAATG CCCCTTGAG 8200  
GGTCCGCTTA TCGGTAGCTA CACAGGCCCT TCTGATTGAC GTTGGGTGAG 8250

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CCTCCCGTAG TCTTCCTGGG CCCCTGGAG GTACATGTCC CCCAGCATTG 8300.

GTTGAAAGAGC TTCAGCCAAG AGTTACACAT AAAGGCCATG TTGTGTTGCA 8350

GTCACACAGAC TGCAAAAGTCT GCTCCAGGAT GAAAGCCACT CAGTGTGGC 8400

AAATGTGCAC ATTCATTTAT AAGGATGTCA ACTACAGTCA GAGAACCCCT 8450

TTGTGTTGG TCCCCCCCCTG TGTCACATGT GGAACAGGGC CCAGTTGGCA 8500

AGTTGTACCA ACCAACTGAA GGGATTACAT GCACGTCCCC 8540

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer UDEC690

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCTGCAGG ACATCCAGAT GACTCACTT 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

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- (A) DESCRIPTION: Oligonucleotide primer UDEC395  
(iii) HYPOTHETICAL: No  
(iv) ANTI-SENSE: Yes

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA . . . . . 30

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 747 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: 5g1.1M1 scFv (murine)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GCC GAC ATC CAG ATG ACT .CAG TCT CCA 30  
Met Ala Asp Ile Gln Met Thr .Gln Ser Pro  
1 5 10

GCT TCA CTG TCT GCA TCT GTG GGA GAA ACT 60  
Ala Ser Leu Ser Ala Ser Val Gly Glu Thr  
15 20

GTC ACC ATC ACA TGT GGA GCA AGT GAG AAT 90  
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn  
25 30

ATT TAC GGT TTA AAT TGG TAT CAG CGG 120  
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg  
35 40

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AAA CAG GGA AAA TCT CCT CAG CTC CTG ATG 150  
Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile  
45 50

TAT GGT GCA ACC AAC TTG GCA GAT GGC ATG 180  
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met  
55 60

TCA TCG AGG TTC AGT GGC AGT GGA TCT GGT 210  
Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly  
65 70

AGA CAG TAT TAT CTC AAC ATC AGT AGC CTG 240  
Arg Gln Tyr Tyr Leu Lys Ile Ser Ser Leu  
75 80

CAT CCT GAC GAT GTT GCA ACG TAT TAC TGT 270  
His Pro Asp Asp Val Ala Thr Tyr Tyr Cys  
85 90

CAA AAT GTG TTA AAT ACT CCT CTC ACG TTC 300  
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe  
95 100

GGT GCT GGG ACC AAG TTG GAG CTG AAA CGG 330  
Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
105 110

ACC GGA GGT GGC GGG TCG CAG GGT CAG CTG 360  
Thr Gly Gly Gly Ser Gly Gly Gly  
115 120

TCG GGT GGC GGA GGG TCG CAG GGT CAG CTG 390  
Ser Gly Gly Gly Ser Gln Val Gln Leu  
125 130

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CAG CAG TCT GGA GCC GAG CTG ATG AAG CCT 420  
Gln Gln Ser Gly Ala Glu Leu Met Lys Pro  
135 140

GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT 450  
Gly Ala Ser Val Lys Met Ser Cys Lys Ala  
145 150

ACT GGC TAC ATA TTC AGT AAC TAC TGG ATA 480  
Thr Gly Tyr Ile Phe Ser Asn Tyr Trp Ile  
155 160

CAG TGG ATA AAG CAG AGG CCT GGA CAT GGC 510  
Gln Trp Ile Lys Gln Arg Pro Gly His Gly  
165 170

CTT GAG TGG ATT GGT GAG ATT TTA CCT GGA 540  
Leu Glu Trp Ile Gly Glu Ile Leu Pro Gly  
175 180

AGT GGT TCT ACT GAG TAC ACT GAG AAC TTC 570  
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe  
185 190

AAG GAC AAG GCC GCA TTC ACT GCA GAT ACA 600  
Lys Asp Lys Ala Ala Phe Thr Ala Asp Thr  
195 200

TCC TCC AAC ACA GCC TAC ATG CAA CTC AGC 630  
Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser  
205 210

AGC CTG ACA TCA GAG GAC TCT GCC GTC TAT 660  
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
215 220

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TAC TGT GCA AGA TAT TTC TTC GGT AGT AGC 690  
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
225 230

CCC AAC TGG TAC TTC GAT GTC TGG GCC GCA 720  
Pro Asn Trp Tyr Phe Asp Val Trp Gly Ala  
235 240

GGG ACC ACG GTC ACC GTC TCC TCA TGA 747  
Gly Thr Thr Val Thr Val Ser Ser  
245

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv CB (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CGG 30  
Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90  
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn  
25 30

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ATC TAT GGC GCG CTG AAC TGG TAT CAA CGT 120  
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg  
35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180  
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val  
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240  
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270  
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
85 90

CGG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300  
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe  
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330  
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360  
Thr Gly Gly Gly Ser Gly Gly Gly Gly  
115 120

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TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390.  
Ser Gly Gly Gly Ser Gln Val Gln Leu  
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420  
Val..Gln Ser Gly Ala Glu Val Lys Lys Pro  
135 140

GCG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450.  
Gly Ala Ser..Val Lys Val Ser Cys Lys Ala  
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480.  
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile  
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510.  
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly  
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540  
Leu Glu Trp Met Gly Glu Ile..Leu Pro Gly  
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570  
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe  
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600.  
Lys Asp Arg Val Thr Met Thr Arg Asp Thr  
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630  
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser  
205 210

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AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660  
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
Gly Thr Leu Val Thr Val Ser Ser  
245

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1M1 VL HuK (chimeric light chain)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30  
Met Gly Ile Gln Gly Gly Ser Val Leu Phe  
-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TCC 60  
Gly Leu Leu Leu Val Leu Ala Val Phe Cys  
-15 -10

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CAT TCA GGT CAT AGC CTG CAG GAC ATC CAG 90  
His Ser Gly His Ser Leu Gln Asp Ile Gln  
-5 1 5

ATG ACT CAG TCT CCA GCT TCA CTG TCT GCA 120  
Met Thr Gln Ser Pro Ala Ser Leu Ser Ala  
10 15

TCT GGG GGA GAA ACT GTC ACC ATC ACA TGT 150  
Ser Val Gly Glu Thr Val Thr Ile Thr Cys  
20 25

GGA GCA AGT GAG AAT ATT TAC GGT GCT TTA 180  
Gly Ala Ser Gln Asn Ile Tyr Gly Ala Leu  
30 35

AAT TGG TAT CAG CGG AAA CAG GGA AAA TCT 210  
Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser  
40 45

CCT CAG CTC CTG ATC TAT GGT GCA ACC AAC 240  
Pro Gln Leu Leu Ile Tyr Gly Ala Thr Asn  
50 55

TTG GCA GAT GGC ATG TCA TCG AGG TTC AGT 270  
Leu Ala Asp Gly Met Ser Ser Arg Phe Ser  
60 65

GGC AGT GGA TCT GGT AGA CAG TAT TAT CTC 300  
Gly Ser Gln Ser Gly Arg Gln Tyr Tyr Leu  
70 75

AAG ATC AGT AGC CTG CAT CCT GAC GAT GTT 330  
Lys Ile Ser Ser Leu His Pro Asp Asp Val  
80 85

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GCA ACG TAT TAC TGT CAA AAT GTG TTA AAT 360  
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn  
90 95

ACT CCT CTC ACG TTC GGT GCT GGG ACC AAG 390  
Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys  
100 105

TTG GAG CTG AAA CGA ACT GTG GCT GCA CCA 420  
Leu Glu Leu Lys Arg Thr Val Ala Ala Pro  
110 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450  
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
120 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480  
Gln Leu Lys Ser Gly Thr Ala Ser Val Val  
130 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510  
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
140 145

GCC AAA CTA CAG TGG AAG GTG GAT AAC GCC 540  
Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
150 155

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570  
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
160 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600  
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr  
170 175

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AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630  
 Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 180 185

GCA GAC TAC GAG AAA TAC AAA GTC TAC GCC 660.  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
 190 195

TGC GAA GTC ACC CAT CAG GCC CTG AGC TCG 690  
 Cys Glu Val Thr His Gin Gly Leu Ser Ser  
 200 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720  
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
 210 215

TGT TAG 726  
 Cys

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid  
 (A) DESCRIPTION: 5G1.1M1 VH +HuG1 (chimeric Fd)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AAA TGG AGC TGG GTT ATT CTC TTC CTC 30  
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
 -15 -10

CTG TCA GTA ACT GCA GGT GTC CAC TCC CAG 60  
 Leu Ser Val Thr Ala Gly Val His Ser Cln

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GTT CAG CTG CAG CAG TCT GGA GCT GAG CTG 90  
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu  
5 10

ATG AAG CCT GGG GCC TCA GTG AAG ATG TCC 120  
Met Lys Pro Gly Ala Ser Val Lys Met Ser  
15 20

TGC AAG GCT ACT GGC TAC ATA TTC AGT AAC 150  
Cys Lys Ala Thr Gly Tyr Ile Phe Ser Asn  
25 30

TAC TGG ATA CAG TGG ATA AAG CAG AGG CCT 180  
Tyr Trp Ile Gln Trp Ile Lys Gln Arg Pro  
35 40

GGA CAT GGC CTT GAG TGG ATT GGT GAG ATT 210  
Gly His Gly Leu Glu Trp Ile Gly Glu Ile  
45 50

TTA CCT GGA AGT GGT TCT ACT GAG TAC ACT 240  
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr  
55 60

GAG AAC TTC AAG GAC AAG GCC GCA TTC ACT 270  
Glu Asn Phe Lys Asp Lys Ala Ala Phe Thr  
65 70

GCA GAT ACA TCC TCC AAC ACA GCC TAC ATG 300  
Ala Asp Thr Ser Ser Asn Thr Ala Tyr Met  
75 80

CAA CTC AGC AGC CTG ACA TCA GAG GAC TCT 330  
Gln Leu Ser Ser Lys Thr Ser Glu Asp Ser  
85 90

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GCC GTC TAT TAC TGT GCA AGA TAT TTC TTC 360  
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe  
95 100

GGT AGT AGC CCC AAC TGG TAC GAT GTC 390  
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val  
105 110

TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC 420  
Trp Gly Ala Gly Thr Thr Val Thr Val Ser  
115 120

TCA GCC TCC ACC AAG GGC CCA TOG GTC TTC 450  
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
125 130

CCC CTG GCG CCC TCC TCC RAG AGC ACC TCT 480  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
135 140

GCG GGC ACA GCG GCC CTG GGC TCC CTG GTC 510  
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540  
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
155 160

TOG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570  
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
165 170

GTC CAC ACC TTC CCG GCT GTC CTA CAG TCC 600  
Val His Thr Phe Pro Ala Val Leu Gln Ser  
175 180

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TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630  
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660  
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
195 200

ACC TAC ATC TCG AAC GTG AAT CAC AAG CCC 690  
Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720  
Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750  
Pro Lys Ser Cys Asp Lys Thr His Thr  
225

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRL (Humanized Fd)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30  
Met Lys Trp Ser Trp Val Ile Leu Phe Leu

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CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60  
Leu Ser Val Thr Ala Gly Val His Ser Gln  
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90  
Val Gln Leu Val Gln Ser Gly Ala Glu Val  
5 10

AAG AAG CCA GGG GCC TCA GTC AAA GAG TCC 120  
Lys Lys Pro Gly Ala Ser Val Lys Val Ser  
15 20

TGT AAA CCT AGC GGC TAT ATT TTT TCT AAT 150  
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn  
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180  
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro  
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210  
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile  
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT GCC 240  
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala  
55 60

CAA AAA TTC CAG GGC CGT GTT ACT ATG ACT 270  
Gln Lys Phe Gln Gly Arg Val Thr Met Thr  
65 70

GCG GAC ACT TCG ACT AGT ACA GCC TAC ATG 300  
Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met  
75 80

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GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330  
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr ...  
 85 90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360  
 Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe  
 95 100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390  
 Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val  
 105 110

TGG GGT CAA GGG ACC CTG GTC ACT GTC TCG 420  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 115 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450  
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe ...  
 125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480  
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 135 140

GGG GGC ACA CGG GCC CTG GGC TGC CTG GTC 510  
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
 145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540  
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 155 160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
 165 170

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GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600  
Val His Thr Phe Pro Ala Val Leu Gln Ser  
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630  
Ser Gly Leu Tyr Ser Ser Leu Ser Val Val  
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660  
Thr Val Pro Ser Ser Leu Gly Thr Gln  
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690  
Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720  
Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750  
Pro Lys Ser Cys Asp Lys Thr His Thr  
225 230

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid
- (A) DESCRIPTION: 5G1.1 VH + IGHRLC (Humanized Fd)

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30  
Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
-15 -10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60  
Leu Ser Val Thr Ala Gly Val His Ser Gln  
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90  
Val Gln Leu Val Gln Ser Gly Ala Glu Val  
5 10

AAG AAG CCA CGG GCC TCA GTC AAA GTG TCC 120  
Lys Lys Pro Gly Ala Ser Val Lys Val Ser  
15 20

TGT AAA GCT AGC GCC TAT ATT TTT TCT AAT 150  
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn  
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180.  
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro  
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210  
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile  
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT ACC 240  
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr  
55 60

GAA AAT TTT AAA GAC CGT GTT ACT ATG ACG 270  
Glu Asn Phe Lys Asp Arg Val Thr Met Thr  
65 70

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CGT GAC ACT TCG ACT AGT ACA GTA TAC ATG 300  
Arg Asp Thr Ser Thr Ser Thr Val Tyr Met  
75   80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330  
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr  
85   90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360  
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe  
95   100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390  
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val  
105   110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
115   120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TCT 450  
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
125   130

CCC CTG GCG CCC TCC TCC ARG AGC ACC TCT 480  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
135   140

GGG GGC ACA GCG GGC CTG GGC TGC CTG GTC 510  
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
145   150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540  
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
155   160

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TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570  
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
165 170

GTC CAC ACC TTC CCG GCT GTC CTA CAG TCC 600  
Val His Thr Phe Pro Ala Val Leu Gln Ser  
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630  
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660  
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690  
Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720  
Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750  
Pro Lys Ser Cys Asp Lys Thr His Thr  
225 230

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5Gl.1 VL +KLV56  
(Humanized light chain)

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30  
Met Gly Ile Gln Gly Gly Ser Val Leu Phe  
-25   -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60  
Gly Leu Leu Leu Val Leu Ala Val Phe Cys  
-15   -10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90  
His Ser Gly His Ser Leu Gln Asp Ile Gln  
-5    1                                       5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120  
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
10   15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys  
20   25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180  
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu  
30   35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210  
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala  
40   45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240  
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn  
50   55

CTG GCA GAT GGA GTC CCT TCT GTC CGC TTC TCT 270  
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser  
60   65